

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/126,505

#7

DATE: 04/01/94
TIME: 14:46:49

INPUT SET: S7711.raw

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Atkinson, John P.
Hourcade, Dennis
Krych, Malgorzata(ii) TITLE OF INVENTION: MODIFIED TRUNCATED COMPLEMENT SYSTEM
REGULATORS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 1100 Peachtree Street, Suite 2800
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30309-4530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/126,505
(B) FILING DATE: 24-SEP-1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/695,514
(B) FILING DATE: 03-MAY-1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: WU101CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (404)-815-6508
(B) TELEFAX: (404)-815-6555

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid

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52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: protein

56

57 (iii) HYPOTHETICAL: NO

58

59 (iv) ANTI-SENSE: NO

60

61 (v) FRAGMENT TYPE: N-terminal

62

63 (x) PUBLICATION INFORMATION:

64 (A) AUTHORS: Hourcade, D. et al.,

65 (C) JOURNAL: J. Exp. Med.

66 (D) VOLUME: 168

67 (F) PAGES: 1255-1270

68 (G) DATE: 1988

69 (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 60

70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

72

73 Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu

74 1 5 10 15

75

76 Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys

77 20 25 30

78

79 Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn

80 35 40 45

81

82 Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg

83 50 55 60

84

85 (2) INFORMATION FOR SEQ ID NO:2:

86

87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 60 amino acids

89 (B) TYPE: amino acid

90 (C) STRANDEDNESS: single

91 (D) TOPOLOGY: linear

92

93 (ii) MOLECULE TYPE: protein

94

95 (iii) HYPOTHETICAL: NO

96

97 (iv) ANTI-SENSE: NO

98

99 (v) FRAGMENT TYPE: N-terminal

100

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

102

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```

103   His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
104   1              5              10              15
105
106   Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
107              20              25              30
108
109   Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
110              35              40              45
111
112
113   Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
114              50              55              60
115

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

134   Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
135   1              5              10              15
136
137   Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
138              20              25              30
139
140   Gly Tyr Arg Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly
141              35              40              45
142
143   Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg
144              50              55              60
145

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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154 (ii) MOLECULE TYPE: protein
155
156 (iii) HYPOTHETICAL: NO
157
158 (iv) ANTI-SENSE: NO
159
160 (v) FRAGMENT TYPE: N-terminal
161
162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
163
164 Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
165 1 5 10 15
166
167 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
168 20 25 30
169
170 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
171 35 40 45
172
173 Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
174 50 55 60
175
176 (2) INFORMATION FOR SEQ ID NO:5:
177
178 (i) SEQUENCE CHARACTERISTICS:
179 (A) LENGTH: 8 amino acids
180 (B) TYPE: amino acid
181 (C) STRANDEDNESS: single
182 (D) TOPOLOGY: linear
183
184 (ii) MOLECULE TYPE: protein
185
186 (iii) HYPOTHETICAL: NO
187
188 (iv) ANTI-SENSE: NO
189
190 (v) FRAGMENT TYPE: N-terminal
191
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
193
194 Asp Lys Lys Ala Pro Ile Cys Asp
195 1 5
196
197 (2) INFORMATION FOR SEQ ID NO:6:
198
199 (i) SEQUENCE CHARACTERISTICS:
200 (A) LENGTH: 8 amino acids
201 (B) TYPE: amino acid
202 (C) STRANDEDNESS: single
203 (D) TOPOLOGY: linear
204

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205 (ii) MOLECULE TYPE: protein
206
207 (iii) HYPOTHETICAL: NO
208
209 (iv) ANTI-SENSE: NO
210
211 (v) FRAGMENT TYPE: N-terminal
212
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
214
215 Ser Asp Pro Leu Pro Glu Cys Arg
216 1 5
217
218 (2) INFORMATION FOR SEQ ID NO:7:
219
220 (i) SEQUENCE CHARACTERISTICS:
221 (A) LENGTH: 4 amino acids
222 (B) TYPE: amino acid
223 (C) STRANDEDNESS: single
224 (D) TOPOLOGY: linear
225
226 (ii) MOLECULE TYPE: protein
227
228 (iii) HYPOTHETICAL: NO
229
230 (iv) ANTI-SENSE: NO
231
232 (v) FRAGMENT TYPE: N-terminal
233
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
235
236 Ser Ser Val Gln
237 1
238
239 (2) INFORMATION FOR SEQ ID NO:8:
240
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 12 amino acids
243 (B) TYPE: amino acid
244 (C) STRANDEDNESS: single
245 (D) TOPOLOGY: linear
246
247 (ii) MOLECULE TYPE: protein
248
249 (iii) HYPOTHETICAL: NO
250
251 (iv) ANTI-SENSE: NO
252
253 (v) FRAGMENT TYPE: N-terminal
254
255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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256
257 Ser Asp Pro Leu Pro Glu Cys Arg Ser Ser Val Gln
258 1 5 10
259

260 (2) INFORMATION FOR SEQ ID NO:9:

261
262 (i) SEQUENCE CHARACTERISTICS:
263 (A) LENGTH: 12 amino acids
264 (B) TYPE: amino acid
265 (C) STRANDEDNESS: single
266 (D) TOPOLOGY: linear
267

268 (ii) MOLECULE TYPE: protein
269

270 (iii) HYPOTHETICAL: NO
271

272 (iv) ANTI-SENSE: NO
273

274 (v) FRAGMENT TYPE: N-terminal
275

276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

277
278 Ser Thr Lys Pro Pro Ile Cys Gln Asn Ala Ala His
279 1 5 10
280

281 (2) INFORMATION FOR SEQ ID NO:10:

282
283 (i) SEQUENCE CHARACTERISTICS:
284 (A) LENGTH: 8 amino acids
285 (B) TYPE: amino acid
286 (C) STRANDEDNESS: single
287 (D) TOPOLOGY: linear
288

289 (ii) MOLECULE TYPE: protein
290

291 (iii) HYPOTHETICAL: NO
292

293 (iv) ANTI-SENSE: NO
294

295 (v) FRAGMENT TYPE: N-terminal
296

297
298
299
300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
301

302 Gln Pro Tyr Ile Thr Gln Asn Tyr
303 1 5
304

305 (2) INFORMATION FOR SEQ ID NO:11:

306

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307 (i) SEQUENCE CHARACTERISTICS:
308 (A) LENGTH: 43 amino acids
309 (B) TYPE: amino acid
310 (C) STRANDEDNESS: single
311 (D) TOPOLOGY: linear
312
313 (ii) MOLECULE TYPE: protein
314
315 (iii) HYPOTHETICAL: NO
316
317 (iv) ANTI-SENSE: NO
318
319 (v) FRAGMENT TYPE: N-terminal
320
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
322
323 Thr Arg Thr Thr Phe His Leu Gly Arg Lys Cys Ser Thr Ala Val Ser
324 1 5 10 15
325
326 Pro Ala Thr Thr Ser Glu Gly Leu Arg Leu Cys Ala Ala His Pro Arg
327 20 25 30
328
329 Glu Thr Gly Ala Leu Gln Pro Pro His Val Lys
330 35 40
331

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/126,505*

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< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/126,505

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INPUT SET: S7711.raw

Line	Original Text	Corrected Text
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